

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):



- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

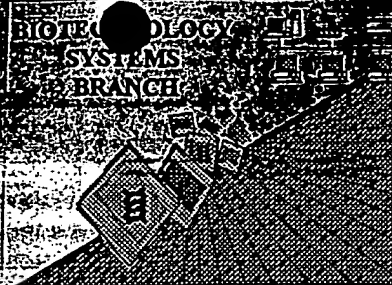
Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

BEST AVAILABLE

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/530,685

Source: Batch

Date Processed by STIC: 10-31-00

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with formal and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/530, 685

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleicls The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☒ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xl) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

BATCH

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/530,685
 DATE: 10/31/2000
 FILE: 11151001

Input Seq : A:\ES.LXC
 Output Seq : B:\CRF3\10312000\1510685.raw

4 <110> APPLICANT: DAIKONG PHARMACEUTICAL CO., LTD. et al.
 6 <120> TITLE OF INVENTION: A Fusion Protein of BEGF AND HUMAN ANGIOGENIN
 AND PROCESS FOR PREPARATION OF SAME
 9 <130> FILE REFERENCE: P5811/00
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/530,685
 C--> 11 <141> CURRENT FILING DATE: 2000-07-13
 11 <150> PRIORITY APPLICATION NUMBER: EP 1997-00641
 12 <151> PRIORITY FILING DATE: 1997-11-11
 14 <160> NUMBER OF SEQ ID NOS: 12
 17 <170> SOFTWARE: KOPATIN 1.5

Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 369
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 23 <400> SEQUENCE: 1
 W--> 25 caggataact ccagggtacac acacttccctg acccagcact
 W--> 26 atgatgccaa accacagggc cgggatgaca gatactgtga
 W--> 27 aagcatcatg aggagacggg gcctgacctc accctgcaaa
 W--> 28 gacatcaaca catttattca tggcaacaag cgcagcatca
 W--> 29 aggccatctg tgaaaacaag aatggaaacc ctcacagaya
 W--> 30 aaacctgaaga ataagcaagt ctctcttcca ggccaccact
 W--> 31 tgcaagctac atggagggtc cccctggcct ccattgccagt
 W--> 32 accgagccac agcgggggtc agaaacgttg ttgttgcttg
 W--> 33 tgaaaatggc ttacctgtcc acctggatca gtcaattttc
 E--> 34 cgctgctcg 369
 37 <210> SEQ ID NO: 2
 38 <211> LENGTH: 123
 39 <212> TYPE: PPT
 40 <213> ORGANISM: Homo sapiens
 42 <400> SEQUENCE: 2
 43 Gln Asp Asn Ser Arg Tyr Thr His Phe Leu Thr
 E--> 44 Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp
 E--> 45 His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp
 E--> 46 Arg Tyr Cys Glu Ser Ile Met Arg Arg Arg Gly Leu
 E--> 47 Tyr Cys Glu Ser Ile Met Arg Arg Arg Gly Leu
 E--> 48 Thr Ser Pro Cys Lys Asp Ile Asn Thr Phe Ile His
 E--> 49 Ser Pro Cys Lys Asp Ile Asn Thr Phe Ile His
 E--> 50 Gly Asn Lys Arg Ser Ile Lys Ala Ile Cys Glu Asn
 E--> 51 Asn Lys Arg Ser Ile Lys Ala Ile Cys Glu Asn
 E--> 52 Lys Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile
 E--> 53 Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile
 E--> 54 Ser Lys Ser Ser Phe Gln Val Thr Thr Cys Lys Leu
 E--> 55 Lys Ser Ser Phe Gln Val Thr Thr Cys Lys Leu

incorrect nucleic acid
 sequence format. See
 p. 13 for clarification.

Amino acids "wrapped"
 down to next line. See
 #2 on Error Summary
 Sheet.

There is also an amino acid
 sequence format error. See p. 14
 for a clarification.

The types of errors shown exist throughout the Sequence Listing. Please check
 subsequent sequences for similar errors.

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/530,685

DATE: 10/31/2000
 TIME: 11:51:01

Input Seq : A:\ES.txt
 Output Seq: N:\CRF3\10312000\1530685.raw

E--> 56 His
 E--> 57 Gly Gly Ser Pro Trp Pro Pro Cys Gln Tyr Arg
 E--> 58 Ala
 E--> 59 Thr Ala Gly Phe Arg Asn Val Val Val Ala Cys
 E--> 60 Glu
 E--> 61 Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile
 E--> 62 Phe
 E--> 63 Arg Arg Pro

*"wrapped" amino acids
 See previous page*

64 <210> SEQ ID NO: 1
 65 <211> LENGTH: 159
 66 <212> TYPE: CDS
 67 <213> ORGANISM: Homo sapiens
 68 <190> SEQUENCE: 3

W--> 71 aatagtgaact cagaatgccc gctgagccat gacggctact
 W--> 72 gctgcacga cggcgtatgc atgtacatcg aagcactgga
 W--> 73 caaatacgcg tgcaactgtg ttgttgcta catcggcgag
 E--> 74 cgctgtcagt accgtgacct taagtgggtg gaactgcgc

75 <210> SEQ ID NO: 4
 76 <211> LENGTH: 33
 77 <212> TYPE: CDS
 78 <213> ORGANISM: Homo sapiens
 79 <190> SEQUENCE: 4

80 <210> SEQ ID NO: 5
 81 <211> LENGTH: 27
 82 <212> TYPE: CDS
 83 <213> ORGANISM: Artificial Sequence
 84 <220> FEATURE:
 85 <223> OTHER INFORMATION: primer for human angiogenin
 86 <190> SEQUENCE: 5
 E--> 84 Gly
 E--> 85 Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile
 E--> 86 Glu
 E--> 87 Ala Leu Asp Lys Tyr Ala Cys Asn Cys Val Val
 E--> 88 Gly
 E--> 89 Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu
 E--> 90 Lys
 E--> 91 Trp Trp Glu Leu Arg

92 <210> SEQ ID NO: 6
 93 <211> LENGTH: 27
 94 <212> TYPE: CDS
 95 <213> ORGANISM: Artificial Sequence
 96 <220> FEATURE:
 97 <223> OTHER INFORMATION: primer for human angiogenin
 98 <190> SEQUENCE: 6

E--> 102 agaattccagg ataactccag gtacaca
 103 <210> SEQ ID NO: 7
 104 <211> LENGTH: 33
 105 <212> TYPE: CDS
 106 <213> ORGANISM: Artificial Sequence
 107 <220> FEATURE:
 108 <223> OTHER INFORMATION: primer for human angiogenin
 109 <190> SEQUENCE: 7

E--> 114 taagcttacg gaaaattgac tgatcca
 115 <210> SEQ ID NO: 8
 116 <211> LENGTH: 33

RAW SEQUENCE LISTING DATE: 10/31/2000
 PATENT APPLICATION: US/09/530,685 TIME: 11:51:01

Input Set : A:\ES.txt
 Output Set: N:\CRF3\10312000\1530685.raw

```

119 <212> TYPE: DNA
120 <213> ORGANISM: Artificial Sequence
121 <220> FEATURE:
123 <223> OTHER INFORMATION: primer for human angiogenin
125 <400> SEQUENCE: 7
E--> 126      aaccgtggcg caggcccc g ataactccag gta
129 <210> SEQ ID NO: 8
130 <211> LENGTH: 33
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
135 <223> OTHER INFORMATION: primer for human angiogenin
137 <400> SEQUENCE: 8
E--> 138      gcctgcagtt agcccgggcg acggaaaatt gac
141 <210> SEQ ID NO: 9
142 <211> LENGTH: 28
143 <212> TYPE: DNA
144 <213> ORGANISM: Artificial Sequence
146 <220> FEATURE:
147 <223> OTHER INFORMATION: linker for ligating angiogenin and hcc
149 <400> SEQUENCE: 9
E--> 150      ccggggcaata gtgactccga atgtccgc
153 <210> SEQ ID NO: 10
154 <211> LENGTH: 27
155 <212> TYPE: DNA
156 <213> ORGANISM: Artificial Sequence
158 <220> FEATURE:
159 <223> OTHER INFORMATION: oligomer for linker
161 <400> SEQUENCE: 10
E--> 162      tcagcgggaca ttcggagtca ctattgc
165 <210> SEQ ID NO: 11
166 <211> LENGTH: 40
167 <212> TYPE: DNA
168 <213> ORGANISM: Artificial Sequence
170 <220> FEATURE:
171 <223> OTHER INFORMATION: linker for expression vector pTE4082
173 <400> SEQUENCE: 11
E--> 174      ccggggcggcg gccgatccaa tagtgactcc gaatgtccgc
177 <210> SEQ ID NO: 12
178 <211> LENGTH: 39
179 <212> TYPE: DNA
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <223> OTHER INFORMATION: linker for expression vector pTE4082
185 <400> SEQUENCE: 12
E--> 186      tcagcgggaca ttcggagtca ctattggatc cgccgcgcg
189 <210> SEQ ID NO: 13
190 <211> LENGTH: 37
191 <212> TYPE: DNA

```

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/530,685
 DATE: 10/31/2000
 TIME: 11:51:01

Input Set: A:\ES.txt
 Output Set: N:\CRF3\10312000\1530685.raw

```

192 <21> ORGANISM: Artificial Sequence
193 <22> FEATURE:
194 <223> OTHER INFORMATION: primer for 222bp fragment of hlgf gene
195 <400> SEQUENCE: 13
E--> 198      acttaagtgg tgggaactgc gccaggataa ctccagg
201 <210> SEQ ID NO: 13
202 <211> LENGTH: 30
203 <212> TYPE: DNA
204 <213> ORGANISM: Artificial Sequence
205 <220> FEATURE:
206 <223> OTHER INFORMATION: primer for 2929bp of hlgf and 41bp fragment
207      of
208      angiotensin
209      II
210 <400> SEQUENCE: 14
E--> 212      gcctgcaggt tatcacgggc gacggaaaat
215 <210> SEQ ID NO: 15
216 <211> LENGTH: 10
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
220 <223> OTHER INFORMATION: primer for 410bp fragment of angiotensin
221      II
222 <400> SEQUENCE: 15
E--> 224      acttaagtgg tgggaactgc gcggccagga taactccagg
227 <210> SEQ ID NO: 16
228 <211> LENGTH: 33
229 <212> TYPE: DNA
230 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: primer containing NdeI restriction site
233 <400> SEQUENCE: 16
E--> 236      gcgcacatat gcaggataac tccaggtaca cac
239 <210> SEQ ID NO: 17
240 <211> LENGTH: 177
241 <212> TYPE: PR1
242 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: amino acid sequence of fusion protein
245 <400> SEQUENCE: 17
246      Gln Asp Asn Ser Arg Tyr Thr His Phe Leu Thr
E--> 249 Gln
E--> 250      His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp
E--> 251 Arg
E--> 252      Tyr Cys Glu Ser Ile Met Arg Arg Arg Gly Leu
E--> 253 Thr
E--> 254      Ser Pro Cys Lys Asp Ile Asn Thr Phe Ile His
E--> 255 Gly
E--> 256      Asn Lys Arg Ser Ile Lys Ala Ile Cys Glu Asn
E--> 257 Lys
E--> 258      Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile

```

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/530,685
 DATE: 10/31/2000
 TIME: 11:51:01

Input Seq : A:\ES.txt
 Output Seq : N:\CRF3\10312000\1530685.raw

```

E--> 259 Ser
E--> 260 Lys Ser Ser Phe Gln Val Thr Thr Cys Lys Leu
E--> 261 His
E--> 262 Gly Gly Ser Pro Trp Pro Pro Cys Gln Tyr Arg
E--> 263 Ala
E--> 264 Thr Ala Gly Phe Arg Asn Val Val Val Ala Cys
E--> 265 Glu
E--> 266 Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile
E--> 267 Phe
E--> 268 Arg Arg Pro Gly Asn Ser Asp Ser Glu Cys Pro
E--> 269 Leu
E--> 270 Ser His Asp Gly Tyr Cys Leu His Asp Gly Val
E--> 271 Cys
E--> 272 Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys
E--> 273 Asn
E--> 274 Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln
E--> 275 Tyr
E--> 276 Arg Asp Leu Lys Trp Trp Glu Leu Arg
279 <210> SEQ ID NO: 18
280 <211> LENGTH: 181
281 <212> TYPE: PRT
282 <213> ORGANISM: Artificial Sequence
284 <210> FEATURE:
285 <223> OTHER INFORMATION: amino acid sequence of fusion protein
287 <400> SEQUENCE: 18
288 Glu Asp Asn Ser Arg Tyr Phe His Phe Leu Thr
E--> 289 Gln
E--> 290 His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp
E--> 291 Arg
E--> 292 Tyr Cys Glu Ser Ile Met Arg Arg Arg Gly Leu
E--> 293 Thr
E--> 294 Ser Pro Cys Lys Asp Ile Asn Thr Phe Ile His
E--> 295 Gly
E--> 296 Asn Lys Arg Ser Ile Lys Ala Ile Cys Glu Asn
E--> 297 Lys
E--> 298 Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile
E--> 299 Ser
E--> 300 Lys Ser Ser Phe Gln Val Thr Thr Cys Lys Leu
E--> 301 His
E--> 302 Gly Gly Ser Pro Trp Pro Pro Cys Gln Tyr Arg
E--> 303 Ala
E--> 304 Thr Ala Gly Phe Arg Asn Val Val Val Ala Cys
E--> 305 Glu
E--> 306 Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile
E--> 307 Phe
E--> 308 Arg Arg Pro Gly Gly Gly Gly Ser Asn Ser Asp
E--> 309 Ser
E--> 310 Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu
E--> 311 His

```


RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/530,685

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TIME: 11:51:01

Input Seq : A:\ES.txt

Output Seq : N:\CRF3\10312000\1530685.raw

E--> 312 Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp
 E--> 313 Lys
 E--> 314 Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly
 E--> 315 Glu
 E--> 316 Arg Cys Gln Tyr Arg Asp Leu Lys Trp Trp Glu
 E--> 317 Leu
 E--> 318 Arg

311 <210> SEQ ID NO: 19

312 <211> LENGTH: 176

313 <212> TYPE: PRT

314 <213> ORGANISM: Artificial Sequence

W--> 326 <220> FEATURE: amino acid sequence of fusion protein → see p. 15

W--> 328 <223> OTHER INFORMATION:

328 <220> SEQUENCE: 19

329 Arg Ser Asp Ser Glu Cys Pro Leu Ser His Asp

E--> 330 Gly
 E--> 331 Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile
 E--> 332 Glu
 E--> 333 Ala Leu Asp Lys Tyr Ala Cys Asn Cys Val Val
 E--> 334 Gly
 E--> 335 Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu
 E--> 336 Lys
 E--> 337 Trp Trp Glu Leu Arg Gln Asp Asn Ser Arg Tyr
 E--> 338 Thr
 E--> 339 His Phe Leu Thr Gln His Tyr Asp Ala Lys Pro
 E--> 340 Gln
 E--> 341 Gly Arg Asp Asp Arg Tyr Cys Glu Ser Ile Met
 E--> 342 Arg
 E--> 343 Arg Arg Gly Leu Thr Ser Pro Cys Lys Asp Ile
 E--> 344 Asn
 E--> 345 Thr Phe Ile His Gly Asn Lys Arg Ser Ile Lys
 E--> 346 Ala
 E--> 347 Ile Cys Glu Asn Lys Asn Gly Asn Pro His Arg
 E--> 348 Glu
 E--> 349 Asn Leu Arg Ile Ser Lys Ser Ser Phe Gln Val
 E--> 350 Thr
 E--> 351 Thr Cys Lys Leu His Gly Gly Ser Pro Trp Pro
 E--> 352 Pro
 E--> 353 Cys Gln Tyr Arg Ala Thr Ala Gly Phe Arg Asn
 E--> 354 Val
 E--> 355 Val Val Ala Cys Glu Asn Gly Leu Pro Val His
 E--> 356 Leu
 E--> 357 Asp Gln Ser Ile Phe Arg Arg Pro

360 <210> SEQ ID NO: 20

361 <211> LENGTH: 177

362 <212> TYPE: PRT

363 <213> ORGANISM: Artificial Sequence

364 <220> FEATURE:

365 <223> OTHER INFORMATION: amino acid sequence of fusion protein

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/530,685
 DATE: 10/31/2000
 TIME: 11:51:01

Input Seq : A:\ES.EXE
 Output Seq : H:\CRF3\10312000\1530685.raw

```

W--> 367 <400> SEQUENCE: 20
      368      Asn Ser Asp Ser Gln Cys Pro Leu Ser His Asp
E--> 369 Gly
E--> 370      Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile
E--> 371 Glu
E--> 372      Ala Leu Asp Lys Tyr Ala Cys Asn Cys Val Val
E--> 373 Gly
E--> 374      Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu
E--> 375 Lys
E--> 376      Trp Trp Glu Leu Arg Gly Gln Asp Asn Ser Arg
E--> 377 Tyr
E--> 378      Thr His Phe Leu Thr Gln His Tyr Asp Ala Lys
E--> 379 Pro
E--> 380      Gln Gly Arg Asp Asp Arg Tyr Cys Glu Ser Ile
E--> 381 Met
E--> 382      Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys Asp
E--> 383 Ile
E--> 384      Asn Thr Phe Ile His Gly Asn Lys Arg Ser Ile
E--> 385 Lys
E--> 386      Ala Ile Cys Glu Asn Lys Asn Gly Asn Pro His
E--> 387 Arg
E--> 388      Glu Asn Leu Arg Ile Ser Lys Ser Ser Phe Gln
E--> 389 Val
E--> 390      Thr Thr Cys Lys Leu His Gly Gly Ser Pro Trp
E--> 391 Pro
E--> 392      Pro Cys Gln Tyr Arg Ala Thr Ala Gly Phe Arg
E--> 393 Asn
E--> 394      Val Val Val Ala Cys Glu Asn Gly Leu Pro Val
E--> 395 His
E--> 396      Leu Asp Gln Ser Ile Phe Arg Arg Pro
      399 <210> SEQ ID NO: 21
      400 <211> LENGTH: 131
      401 <212> TYPE: PRT
      402 <213> ORGANISM: Artificial Sequence
      404 <220> FEATURE:
      405 <223> OTHER INFORMATION: amino acid sequence of fusion protein
      407 <400> SEQUENCE: 21
      408      Asn Ser Asp Ser Gln Cys Pro Leu Ser His Asp
E--> 409 Gly
E--> 410      Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile
E--> 411 Glu
E--> 412      Ala Leu Asp Lys Tyr Ala Cys Asn Cys Val Val
E--> 413 Gly
E--> 414      Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu
E--> 415 Lys
E--> 416      Trp Trp Glu Leu Arg Gly Gly Gly Gly Ser Gln
E--> 417 Asp
E--> 418      Asn Ser Arg Tyr Thr His Phe Leu Thr Gln His
E--> 419 Tyr

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/00/530,685

DATE: 10/31/2000

TIME: 11:01:01

Input Seq.: A:\ES.txt

Output Seq.: H:\CRF3\10312000\1530685.raw

```

E--> 420      Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg Tyr
E--> 421 Cys
E--> 422      Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser
E--> 423 Pro
E--> 424      Cys Lys Asp Ile Asn Thr Phe Ile His Gly Asn
E--> 425 Lys
E--> 426      Arg Ser Ile Lys Ala Ile Cys Glu Asn Lys Asn
E--> 427 Gly
E--> 428      Asn Pro His Arg Glu Asn Leu Arg Ile Ser Lys
E--> 429 Ser
E--> 430      Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly
E--> 431 Gly
E--> 432      Ser Pro Trp Pro Pro Cys Gln Val Thr Thr Cys
E--> 433 Ala
E--> 434      Gly Phe Arg Asn Val Val Val Ala Cys Glu Asn
E--> 435 Gly
E--> 436      Leu Pro Val His Leu Asp Gln Ser Ile Phe Arg
E--> 437 Arg
E--> 438      Pro
      441 <210> SEQ ID NO: 22
      442 <211> LENGTH: 186
      443 <212> TYPE: PRT
      444 <213> ORGANISM: Artificial Sequence
      445 <220> FEATURE:
      447 <223> OTHER INFORMATION: amino acid sequence of fusion protein
      449 <400> SEQUENCE: 22
      450      ASD Ser Asp Ser Glu Cys Pro Leu Ser His Asp
E--> 451 Gly
E--> 452      Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile
E--> 453 Glu
E--> 454      Ala Leu Asp Lys Tyr Ala Cys Asn Cys Val Val
E--> 455 Gly
E--> 456      Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu
E--> 457 Lys
E--> 458      Trp Trp Glu Leu Arg Gly Gly Gly Gly Ser Gly
E--> 459 Gly
E--> 460      Gly Gly Ser Gln Asp Asn Ser Arg Tyr Thr His
E--> 461 Phe
E--> 462      Leu Thr Gln His Tyr Asp Ala Lys Pro Gln Gly
E--> 463 Arg
E--> 464      Asp Asp Arg Tyr Cys Glu Ser Ile Met Arg Arg
E--> 465 Arg
E--> 466      Gly Leu Thr Ser Pro Cys Lys Asp Ile Asn Thr
E--> 467 Phe
E--> 468      Ile His Gly Asn Lys Arg Ser Ile Lys Ala Ile
E--> 469 Cys
E--> 470      Glu Asn Lys Asn Gly Asn Pro His Arg Glu Asn
E--> 471 Leu
E--> 472      Arg Ile Ser Lys Ser Ser Phe Gln Val Thr Thr

```

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/530,685
 DATE: 10/31/2000
 TIME: 11:51:01

Input Seq : A:\NES.UXL
 Output Seq : N:\CRF3\0312000\1530685.raw

```

E--> 473 Cys
E--> 474      Lys Leu His Gly Gly Ser Pro Trp Pro Pro Cys
E--> 475 Gln
E--> 476      Val Thr Thr Cys Ala Gly Phe Arg Asn Val Val
E--> 477 Val
E--> 478      Ala Cys Glu Asn Gly Leu Pro Val His Leu Asp
E--> 479 Gln
E--> 480      Ser Ile Phe Arg Arg Pro
183 <210> SEQ ID NO: 24
184 <211> LENGTH: 24
185 <212> TYPE: DNA
186 <213> ORIGIN: Artificial Sequence
188 <220> FEATURE:
189 <221> OTHER INFORMATION: Fusion gene of angiotensin and hEGF
191 <400> SEQUENCE: 25
W--> 492      aatagtgaact cgaatgccc gctgagccat gacggctact
W--> 493      gcctgcacga cggcgatgc atgtacatcg aagcactgga
W--> 494      caaatacgcg tgcactgtg ttgttggtta catcggcgag
W--> 495      cgctgtcagt accgtgacct taagtgggtg gaactgcgcg
W--> 496      gaggaggagg atcccgagg aactccagg acacacactt
W--> 497      cctgacccag cactatgatg ccaaaccaca gggccgggat
W--> 498      gacagatact ytgaaagcat catgaggaga cggggcctga
W--> 499      cctcacctcg caaagacatc aacacattta ttcattggca
W--> 500      caagcgagc atcaaggcca tctgtgaaa caagaatgga
W--> 501      aaccctcaca gaaaaacct aagaataagc aagtcttctt
W--> 502      tccaggtcac cacttgcaag ctacatggag gttccccctg
W--> 503      gcctccatgc cagtaccgag ccacagcggg gttcagaaac
W--> 504      gttgtgtgtg cttgtgaaa tygcttacct gtccacttgg
E--> 505      atcagtcact ttcccgctgc cgg
506 <210> SEQ ID NO: 24
507 <211> LENGTH: 558
510 <212> TYPE: DNA
511 <213> ORIGIN: Artificial Sequence
513 <220> FEATURE:
514 <221> OTHER INFORMATION: Fusion gene of angiotensin and hEGF
516 <400> SEQUENCE: 24
W--> 517      aatagtgaact cgaatgccc gctgagccat gacggctact
W--> 518      gcctgcacga cggcgatgc atgtacatcg aagcactgga
W--> 519      caaatacgcg tgcactgtg ttgttggtta catcggcgag
W--> 520      cgctgtcagt accgtgacct taagtgggtg gaactgcgcg
W--> 521      gaggaggagg atccggagga ggaggatcac aggataactc
W--> 522      caggtagaca cacttccctg cccagcacta tgatgccaaa
W--> 523      ccacagggcc gggatgacag atactgtgaa agcatcatga
W--> 524      ggagacgggg cctgacctca cctgcaaaag acatcaaac
W--> 525      atttatccat ggcaacaagc gcagcatcaa ggccatctgt
W--> 526      gaaaacaaga atggaaaccc tcacagagaa aacctaaaga
W--> 527      taagcaagtc ttctttccag gtcaccactt gcaagctaca
W--> 528      tggaggttcc ccctggcctc catgccagta ccgagccaca
W--> 529      gcggggttca gaaacgttgt tgttgcttgt gaaaatggct

```

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/530,685
 DATE: 10/31/2000
 TIME: 11:51:01

Input Set : A:\ES.txt
 Output Set: N:\CRF3\10312000\1530685.raw

```

E--> 530      tacctgtcca cttggatcag tcaattttcc gtcgcccg
533 <210> SEQ ID NO: 25
534 <211> LENGTH: 30
535 <212> TYPE: DNA
536 <213> ORGANISM: Artificial Sequence
537 <220> FEATURE:
538 <223> OTHER INFORMATION: primer containing BclI restriction site
539 <400> SEQUENCE: 25
E--> 542      ggcgatatga atagtgactc cgaatgtccg
545 <210> SEQ ID NO: 26
546 <211> LENGTH: 26
547 <212> TYPE: DNA
548 <213> ORGANISM: Artificial Sequence
549 <220> FEATURE:
550 <223> OTHER INFORMATION: primer containing BamHI restriction site
551 <400> SEQUENCE: 26
E--> 554      aggatccctcc tcttccgcgc agttccca
557 <210> SEQ ID NO: 27
558 <211> LENGTH: 30
559 <212> TYPE: DNA
560 <213> ORGANISM: Artificial Sequence
561 <220> FEATURE:
562 <223> OTHER INFORMATION: primer containing BamHI restriction site
563 <400> SEQUENCE: 27
E--> 566      cggatccccag gataactcca ggtacacaca
569 <210> SEQ ID NO: 28
570 <211> LENGTH: 35
571 <212> TYPE: DNA
572 <213> ORGANISM: Artificial Sequence
573 <220> FEATURE:
574 <223> OTHER INFORMATION: primer for 415bp DNA fragment
575 <400> SEQUENCE: 28
E--> 578      aggatccgga ggaggaggat cacaggataa ctcca
581 <210> SEQ ID NO: 31
582 <211> LENGTH: 309
583 <212> TYPE: DNA
584 <213> ORGANISM: Artificial Sequence
W--> 650 <220> FEATURE: amino acid sequence of fusion protein → See p. 15
W--> 652 <223> OTHER INFORMATION:
653 <400> SEQUENCE: 31
654 Gln Asp Asn Ser Arg Tyr Thr His Phe Leu Thr
E--> 654 Gln
E--> 655 His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp
E--> 656 Arg
E--> 657 Tyr Cys Glu Ser Ile Met Arg Arg Arg Gly Leu
E--> 658 Thr
E--> 659 Ser Pro Cys Lys Asp Ile Asn Thr Phe Ile His
E--> 660 Gly
E--> 661 Asn Lys Arg Ser Ile Lys Ala Ile Cys Glu Asn

```

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/530,685
 DATE: 10/31/2000
 TIME: 11:51:01

Input Seq : A:\ES.txt
 Output Seq: H:\CRF3\10312000\1530685.raw

```

E--> 662 Lys
E--> 663 Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile
E--> 664 Ser
E--> 665 Lys Ser Ser Phe Gln Val Thr Thr Cys Lys Leu
E--> 666 His
E--> 667 Gly Gly Ser Pro Trp Pro Pro Cys Gln Val Thr
E--> 668 Thr
E--> 669 Cys Ala Gly Phe Arg Asn Val Val Val Ala Cys
E--> 670 Glu
E--> 671 Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile
E--> 672 Phe
E--> 673 Arg Arg Pro Gly Gly Gly Gly Ser Asn Ser Asp
E--> 674 Ser
E--> 675 Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu
E--> 676 His
E--> 677 Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp
E--> 678 Lys
E--> 679 Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly
E--> 680 Glu
E--> 681 Arg Cys Gln Tyr Arg Asp Leu Lys Trp Trp Glu
E--> 682 Leu
E--> 683 Arg Gly Gly Gly Gly Ser Gln Asp Asn Ser Arg
E--> 684 Tyr
E--> 685 Thr His Phe Leu Thr Gln His Tyr Asp Ala Lys
E--> 686 Pro
E--> 687 Gln Gly Arg Asp Asp Arg Tyr Cys Glu Ser Ile
E--> 688 Met
E--> 689 Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys Asp
E--> 690 Ile
E--> 691 Asn Thr Phe Ile His Gly Asn Lys Arg Ser Ile
E--> 692 Lys
E--> 693 Ala Ile Cys Glu Asn Lys Asn Gly Asn Pro His
E--> 694 Arg
E--> 695 Glu Asn Leu Arg Ile Ser Lys Ser Ser Phe Gln
E--> 696 Val
E--> 697 Thr Thr Cys Lys Leu His Gly Gly Ser Pro Trp
E--> 698 Pro
E--> 699 Pro Cys Gln Val Thr Thr Cys Ala Gly Phe Arg
E--> 700 Asn
E--> 701 Val Val Val Ala Cys Glu Asn Gly Leu Pro Val
E--> 702 His
E--> 703 Leu Asp Gln Ser Ile Phe Arg Arg Pro

```

```

706 <210> SEQ ID NO: 32
707 <211> LENGTH: 239
708 <212> TYPE: PRT
709 <213> ORGANISM: Artificial Sequence
711 <220> FEATURE:
712 <223> OTHER INFORMATION: amino acid sequence of fusion protein
714 <400> SEQUENCE: 32

```

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/530,685
 DATE: 10/31/2000
 TIME: 11:01:01

Input Seq : A:\ES.txt
 Output Seq: N:\CRF3\10312000\1530685.raw

```

    716
E--> 716 Gly      Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp
E--> 717          Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile
E--> 718 Glu
E--> 719          Ala Leu Asp Lys Tyr Ala Cys Asn Cys Val Val
E--> 720 Gly
E--> 721          Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu
E--> 722 Lys
E--> 723          Trp Trp Glu Leu Arg Gly Gly Gly Gly Ser Gln
E--> 724 Asp
E--> 725          Asn Ser Arg Tyr Thr His Phe Leu Thr Gln His
E--> 726 Tyr
E--> 727          Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg Tyr
E--> 728 Cys
E--> 729          Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser
E--> 730 Pro
E--> 731          Cys Lys Asp Ile Asn Thr Phe Ile His Gly Asn
E--> 732 Lys
E--> 733          Arg Ser Ile Lys Ala Ile Cys Glu Asn Lys Asn
E--> 734 Gly
E--> 735          Asn Pro His Arg Glu Asn Leu Arg Ile Ser Lys
E--> 736 Ser
E--> 737          Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly
E--> 738 Gly
E--> 739          Ser Pro Trp Pro Pro Cys Gln Val Thr Thr Cys
E--> 740 Ala
E--> 741          Gly Phe Arg Asn Val Val Val Ala Cys Glu Asn
E--> 742 Gly
E--> 743          Leu Pro Val His Leu Asp Gln Ser Ile Phe Arg
E--> 744 Arg
E--> 745          Pro Gly Gly Gly Gly Ser Asn Ser Asp Ser Glu
E--> 746 Cys
E--> 747          Pro Leu Ser His Asp Gly Tyr Cys Leu His Asp
E--> 748 Gly
E--> 749          Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr
E--> 750 Ala
E--> 751          Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg
E--> 752 Cys
E--> 753          Gln Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg

```

Sequence #1

<210> 1
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 1

caggataact	ccaggtacac	acacttcctg	acccagcact	40
atgatgccaa	accacagggc	cgggatgaca	gatactgtga	80
aagcatcatg	aggagacggg	gcctgacctc	accctgcaaa	120
gacatcaaca	catttattca	tggcaacaag	cgcagcatca	160
aggccatctg	tgaaaacaag	aatggaaacc	ctcacagaga	200
aaacctaaga	ataagcaagt	cttctttcca	ggtcaccact	240
tgcaagctac	atggagggtc	cccctggcct	ccatgccagt	280
accgagccac	agcgggggtc	agaaacgttg	ttgttgcttg	320
tgaaaatggc	ttacctgtcc	acttgatca	gtcaattttc	360
cgtcgtccg	369			369

Each line must
 have a cumulative
 total following
 it. (For nucleic
 base

You may have up
 to 6 groups of
 10 nucleic bases
 per row

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p. 14

<210> 4 Sequence #4
 <211> 53
 <212> PRT
 <213> Homo sapiens

<400> 4
 Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly
 1 5 10
 Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu
 15 20
 Ala Leu Asp Lys Tyr Ala Cys Asn Cys Val Val Gly
 25 30 35
 Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys
 40 45
 Trp Trp Glu Leu Arg
 50

Amino acids are
 to be numbered
 underneath each
 5th amino acid.
 You may have up to
 16 amino acids per
 row.

<210> 19 Sequence # 19
<211> 176
<212> PRT
<213> Artificial Sequence

<220> amino acid sequence of fusion protein

<223>



move to here.

<220> is a blank line feature.

This error is also present in
sequence # 31.

VERIFICATION SUMMARY

DATE: 10/31/2000

PATENT APPLICATION: US/09/530,685

TIME: 11:51:02

Input Set : A:\ES.txt

Output Set: N:\CRF3\10312000\1530685.raw

L:11 H:270 C: Current Application Number differs. Replaced Current Application No
L:11 H:271 C: Current Filing Date differs. Replaced Current Filing Date
L:12 H:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:4
L:26 H:336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
L:26 H:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:4
L:27 H:336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
L:27 H:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:4
L:28 H:336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
L:28 H:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:4
L:29 H:336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
L:29 H:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:4
L:30 H:336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
L:30 H:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:4
L:31 H:336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
L:31 H:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:4
L:32 H:336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
L:32 H:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:4
L:33 H:336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
L:33 H:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:4
L:34 H:252 E: No. of Seq. differs. <211>LENGTH:Input:369 Found:9 SEQ:1
L:34 H:252 E: No. of Seq. differs. <211>LENGTH:Input:369 Found:9 SEQ:1
L:41 H:332 E: (32) Invalid/Missing Amino Acid Numbering. SEQ ID:2
H:332 Repeated in SeqNo:2
L:71 H:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:4
L:72 H:336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:3
L:72 H:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:4
L:73 H:336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:3
L:73 H:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:4
L:74 H:336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:3
L:74 H:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:4
L:74 H:252 E: No. of Seq. differs. <211>LENGTH:Input:159 Found:0 SEQ:3
L:84 H:332 E: (32) Invalid/Missing Amino Acid Numbering. SEQ ID:4
H:332 Repeated in SeqNo:4
L:102 H:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:3
L:102 H:252 E: No. of Seq. differs. <211>LENGTH:Input:27 Found:5 SEQ:5
L:114 H:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:3
L:114 H:252 E: No. of Seq. differs. <211>LENGTH:Input:27 Found:0 SEQ:6
L:126 H:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:4
L:126 H:252 E: No. of Seq. differs. <211>LENGTH:Input:33 Found:0 SEQ:7
L:138 H:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:4
L:138 H:252 E: No. of Seq. differs. <211>LENGTH:Input:33 Found:0 SEQ:8
L:150 H:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:3
L:150 H:252 E: No. of Seq. differs. <211>LENGTH:Input:28 Found:0 SEQ:9
L:162 H:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:3
L:162 H:252 E: No. of Seq. differs. <211>LENGTH:Input:27 Found:0 SEQ:10
L:174 H:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:4
L:174 H:252 E: No. of Seq. differs. <211>LENGTH:Input:40 Found:0 SEQ:11
L:186 H:334 W: (2) Invalid Amino Acid in Coding Region. NUMBER OF INVALID KEYS:4

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/530,685

DATE: 10/31/2000

TIME: 11:51:02

Input Set : A:\ES.txt

Output Set : N:\CRF3\10312000\1530685.raw

L:186 H:257 E: No. of Seq. Differs. - 211-LEGGId:Input:39 Found:0 Seq:12
 L:189 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
 L:191 H:251 E: No. of Seq. Differs. - 211-LEGGId:Input:37 Found:0 Seq:13
 L:191 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
 L:211 H:252 E: No. of Seq. Differs. - 211-LEGGId:Input:30 Found:0 Seq:11
 L:224 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
 L:224 H:252 E: No. of Seq. Differs. - 211-LEGGId:Input:40 Found:0 Seq:15
 L:236 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
 L:236 H:252 E: No. of Seq. Differs. - 211-LEGGId:Input:33 Found:0 Seq:16
 L:239 H:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
 H:332 Repeated in SeqNo. 17
 L:289 H:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:18
 H:332 Repeated in SeqNo. 18
 L:324 H:256 W: Invalid Numeric Reader Field, -22> has non-blank data
 L:325 H:258 W: Mandatory Feature missing, -22> OTHER INFORMATION:
 L:336 H:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:19
 H:332 Repeated in SeqNo. 19
 L:367 H:258 W: Missing Blank Line Separator, -430> field identifier
 L:369 H:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:20
 H:332 Repeated in SeqNo. 20
 L:409 H:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:21
 H:332 Repeated in SeqNo. 21
 L:451 H:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
 H:332 Repeated in SeqNo. 22
 L:492 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
 L:493 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
 L:494 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
 L:494 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
 L:494 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
 L:495 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
 L:495 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
 L:496 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
 L:496 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
 L:497 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
 L:497 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
 L:498 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
 L:498 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
 L:499 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
 L:499 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
 L:500 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
 L:500 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
 L:501 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
 L:501 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
 L:502 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
 L:502 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
 L:503 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
 L:503 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
 L:504 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
 L:504 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/530,685

DATE: 10/31/2003

TIME: 11:51:02

Input Set : A:\ES.txt

Output Set: N:\CRF3\10312000\I530685.raw

L:503 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21
 L:505 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID RES:4
 L:505 H:332 E: No. of Seq. differs, <21>LENGTH:Input:41 Found:0 SEQ:21
 L:517 H:321 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID RES:4
 L:518 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21
 L:518 H:314 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID RES:4
 L:519 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21
 L:519 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID RES:4
 L:520 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21
 L:520 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID RES:4
 L:521 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21
 L:521 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID RES:4
 L:522 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21
 L:522 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID RES:4
 L:523 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21
 L:523 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID RES:4
 L:524 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
 L:524 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID RES:4
 L:525 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
 L:525 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID RES:4
 L:526 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
 L:526 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID RES:4
 L:527 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21
 L:527 H:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID RES:4
 L:528 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
 L:529 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
 L:530 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21
 L:530 H:252 E: No. of Seq. differs, <21>LENGTH:Input:558 Found:0 SEQ:24
 L:542 H:252 E: No. of Seq. differs, <21>LENGTH:Input:30 Found:0 SEQ:25
 L:554 H:252 E: No. of Seq. differs, <21>LENGTH:Input:28 Found:0 SEQ:26
 L:566 H:252 E: No. of Seq. differs, <21>LENGTH:Input:30 Found:0 SEQ:27
 L:578 H:252 E: No. of Seq. differs, <21>LENGTH:Input:35 Found:0 SEQ:28
 L:591 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
 L:592 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
 L:593 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
 L:594 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
 L:595 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
 L:596 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
 L:597 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
 L:598 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
 L:599 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
 L:600 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
 L:601 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
 L:602 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
 L:603 H:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
 L:613 H:252 E: No. of Seq. differs, <21>LENGTH:Input:927 Found:0 SEQ:29
 L:642 H:252 E: No. of Seq. differs, <21>LENGTH:Input:717 Found:0 SEQ:30
 L:650 H:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:652 H:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

VERIFICATION SUMMARY DATE: 10/31/2000
PATENT APPLICATION: US/09/530,685 TIME: 11:51:02

Input Set : A:\ES.EXL
Output Set : D:\CRF3\10312000\1530685.raw

Input Set 1: Es (12) FatalId/missing: none Fatal Number: 0 SEQ: 10:31
Data reported in SeqNo: 31
Input Set 2: Es (12) FatalId/missing: none Fatal Number: 0 SEQ: 10:32
Data reported in SeqNo: 32

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